

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 101534002
Source: PCT
Date Processed by STIC: 5/13/15

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 05/13/2005

PATENT APPLICATION: US/10/534,002

TIME: 14:58:59

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\05132005\J534002.raw

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3 <110> APPLICANT: NARIMATSU, Hisashi
4     SATO, Takashi
5     GOTOH, Masanori
7 <120> TITLE OF INVENTION: METHOD OF DETECTING BONE PAGET'S DISEASE
9 <130> FILE REFERENCE: 159-88 / YCT-882
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/534,002
12 <141> CURRENT FILING DATE: 2005-05-05
14 <150> PRIOR APPLICATION NUMBER: PCT/JP2003/014211
15 <151> PRIOR FILING DATE: 2003-11-07
17 <150> PRIOR APPLICATION NUMBER: JP2002-323438
18 <151> PRIOR FILING DATE: 2002-11-07
20 <160> NUMBER OF SEQ ID NOS: 70
22 <170> SOFTWARE: MS Word
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 2649
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(2649)
34 <400> SEQUENCE: 1
35 atg gct gtg cgc tct cgc cgc ccg tgg atg agc gtg gca tta ggg ctg      48
36 Met Ala Val Arg Ser Arg Arg Pro Trp Met Ser Val Ala Leu Gly Leu
37 1          5          10          15
39 gtg ctg ggc ttc acc gcc gcg tcc tgg ctc atc gcc ccc agg gtg gcg      96
40 Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala
41          20          25          30
43 gag ctg agc gag agg aag aga cgt ggc tcc agc ctc tgc tcc tac tac      144
44 Glu Leu Ser Glu Arg Lys Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr
45          35          40          45
47 ggt cgc tct gct gct ggc ccc cgc gcc ggc gct cag cag ccg ctc ccc      192
48 Gly Arg Ser Ala Ala Gly Pro Arg Ala Gly Ala Gln Gln Pro Leu Pro
49          50          55          60
51 cag ccc cag tcc cga cca cgg cag gag cag tcg ccg ccc ccc gcg cgc      240
52 Gln Pro Gln Ser Arg Pro Arg Gln Glu Gln Ser Pro Pro Pro Ala Arg
53 65          70          75          80
55 cag gat ctc cag ggg cca ccg ctg ccc gag gca gca ccc ggg atc acc      288
56 Gln Asp Leu Gln Gly Pro Pro Leu Pro Glu Ala Ala Pro Gly Ile Thr
57          85          90          95
59 agt ttt cga agc agc ccc tgg cag cag cca cct ccg ctg cag cag cgg      336
60 Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Pro Pro Leu Gln Gln Arg
61          100          105          110
63 cgg cga gga cgc gag cct gag ggc gcg acg ggg ctt ccc ggt gct cca      384

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64 Arg Arg Gly Arg Glu Pro Glu Gly Ala Thr Gly Leu Pro Gly Ala Pro
65      115      120      125
67 gcg gcc gag ggg gag ccc gag gag gag gac ggg ggc gcg gct ggg cag      432
68 Ala Ala Glu Gly Glu Pro Glu Glu Glu Asp Gly Gly Ala Ala Gly Gln
69      130      135      140
71 cgg aga gac ggc cgg ccg ggg agt agc cac aac ggc agc ggg gac ggg      480
72 Arg Arg Asp Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly
73 145      150      155      160
75 ggc gct gcc gcc ccg agc gcc cga ccc cgg gac ttc ctg tac gtg ggg      528
76 Gly Ala Ala Ala Pro Ser Ala Arg Pro Arg Asp Phe Leu Tyr Val Gly
77      165      170      175
79 gtg atg acc gcg cag aag tac ctg ggc agc cgc gcg ctg gcc gcg cag      576
80 Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln
81      180      185      190
83 cgg acc tgg gcg cgt ttc atc ccg ggc cgc gtg gag ttc ttt tcc agc      624
84 Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser
85      195      200      205
87 cag cag ccc ccc aac gcc ggc cag ccc ccg cca ccc ctg cct gtc atc      672
88 Gln Gln Pro Pro Asn Ala Gly Gln Pro Pro Pro Pro Leu Pro Val Ile
89      210      215      220
91 gcg cta ccg ggt gtg gac gac tcc tat cct ccc cag aaa aag tcc ttc      720
92 Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
93 225      230      235      240
95 atg atg atc aag tac atg cac gac cac tac ctg gac aag tat gag tgg      768
96 Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu Trp
97      245      250      255
99 ttc atg cgc gcc gac gac gat gtc tac atc aaa ggt gat aaa tta gaa      816
100 Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Lys Leu Glu
101      260      265      270
103 gag ttt ctt aga tcg cta aac agc agt aag cct ctc tac ctg gga cag      864
104 Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu Gly Gln
105      275      280      285
107 act ggc ctg ggg aat att gaa gag ctt gga aag ctg gga ctg gag cct      912
108 Thr Gly Leu Gly Asn Ile Glu Glu Leu Gly Lys Leu Gly Leu Glu Pro
109      290      295      300
111 ggg gaa aac ttc tgt atg gga gga cct ggc atg atc ttt agc cga gaa      960
112 Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser Arg Glu
113 305      310      315      320
115 gtt ctc agg agg atg gtg cca cat att ggt gaa tgc ctt aga gaa atg      1008
116 Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg Glu Met
117      325      330      335
119 tac acg act cat gag gat gtg gaa gta gga aga tgc gtt cgc cgt ttt      1056
120 Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg Arg Phe
121      340      345      350
123 ggt ggg act cag tgt gtc tgg tct tac gag atg caa caa ctg ttc cat      1104
124 Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu Phe His
125      355      360      365
127 gaa aat tat gaa cac aat cgg aag ggt tac atc caa gac ctt cac aat      1152
128 Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu His Asn

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129	370	375	380	
131	agc aaa atc cat gca gcc ata aca ctt cat ccc aac aaa agg cct gca	1200		
132	Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg Pro Ala			
133	385 390 395 400			
135	tac caa tac agg ctg cat aat tac atg ctc agc cgc aaa att tct gaa	1248		
136	Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile Ser Glu			
137	405 410 415			
139	ctt cgc tac cgc acc atc cag ctc cac agg gaa agt gcc ctg atg agc	1296		
140	Leu Arg Tyr Arg Thr Ile Gln Leu His Arg Glu Ser Ala Leu Met Ser			
141	420 425 430			
143	aag ctc agt aac aca gaa gtg agc aaa gag gac cag cag ctg gga gtg	1344		
144	Lys Leu Ser Asn Thr Glu Val Ser Lys Glu Asp Gln Gln Leu Gly Val			
145	435 440 445			
147	ata cct tct ttc aac cac ttc cag cct cgg gag aga aat gaa gtg ata	1392		
148	Ile Pro Ser Phe Asn His Phe Gln Pro Arg Glu Arg Asn Glu Val Ile			
149	450 455 460			
151	gaa tgg gag ttc ctg aca ggg aag ctt cta tac tca gca gct gag aac	1440		
152	Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala Glu Asn			
153	465 470 475 480			
155	cag ccc cct cga cag agc ctc agt agc att tta aga aca gca ctg gat	1488		
156	Gln Pro Pro Arg Gln Ser Leu Ser Ser Ile Leu Arg Thr Ala Leu Asp			
157	485 490 495			
159	gat acc gtc cta cag gtg atg gag atg atc aat gag aat gcc aag agc	1536		
160	Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala Lys Ser			
161	500 505 510			
163	aga gga cgg ctc att gac ttc aag gaa att cag tat ggc tac cgc aga	1584		
164	Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr Arg Arg			
165	515 520 525			
167	gtt aac ccc atg cac ggg gtg gag tac att ttg gat tta ctc ctt tta	1632		
168	Val Asn Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu Leu Leu			
169	530 535 540			
171	tac aaa aga cac aag gga agg aaa ctg act gtg cca gtg aga cgt cat	1680		
172	Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg Arg His			
173	545 550 555 560			
175	gcc tat ctt cag cag ttg ttc agc aag cct ttc ttc aga gag acc gaa	1728		
176	Ala Tyr Leu Gln Gln Leu Phe Ser Lys Pro Phe Phe Arg Glu Thr Glu			
177	565 570 575			
179	gag cta gat gtc aac agt ctt gtg gag agt att aac agt gaa act cag	1776		
180	Glu Leu Asp Val Asn Ser Leu Val Glu Ser Ile Asn Ser Glu Thr Gln			
181	580 585 590			
183	tca ttc tcc ttt ata tct aat tct tta aag ata tta tct tct ttt caa	1824		
184	Ser Phe Ser Phe Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser Phe Gln			
185	595 600 605			
187	ggt gcc aaa gaa atg gga ggg cac aat gaa aag aaa gta cac att ctc	1872		
188	Gly Ala Lys Glu Met Gly Gly His Asn Glu Lys Lys Val His Ile Leu			
189	610 615 620			
191	gtt cct ctc atc gga agg tat gac att ttc ttg aga ttc atg gag aac	1920		
192	Val Pro Leu Ile Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met Glu Asn			
193	625 630 635 640			

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195 ttt gaa aac atg tgt ctt atc cca aag cag aat gta aag ttg gtc att      1968
196 Phe Glu Asn Met Cys Leu Ile Pro Lys Gln Asn Val Lys Leu Val Ile
197          645          650          655
199 atc ctt ttc agt agg gat tct ggc caa gac tcc agc aag cat att gag      2016
200 Ile Leu Phe Ser Arg Asp Ser Gly Gln Asp Ser Ser Lys His Ile Glu
201          660          665          670
203 ctg ata aaa ggg tac cag aac aag tac ccc aaa gca gaa atg acc ctg      2064
204 Leu Ile Lys Gly Tyr Gln Asn Lys Tyr Pro Lys Ala Glu Met Thr Leu
205          675          680          685
207 atc cca atg aag gga gag ttt tcc aga ggt ctt ggt ctt gaa atg gct      2112
208 Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu Met Ala
209          690          695          700
211 tct gcc cag ttt gac aat gac act ttg ctg cta ttt tgt gat gtt gac      2160
212 Ser Ala Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp Val Asp
213 705          710          715          720
215 ttg atc ttc aga gaa gat ttt ctc caa cga tgt aga gac aat aca att      2208
216 Leu Ile Phe Arg Glu Asp Phe Leu Gln Arg Cys Arg Asp Asn Thr Ile
217          725          730          735
219 cag gga caa cag gtg tac tat ccc atc atc ttt agc cag tat gac cca      2256
220 Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr Asp Pro
221          740          745          750
223 aag gta aca aac ggg gga aat cct ccc act gat ggt tac ttc ata ttc      2304
224 Lys Val Thr Asn Gly Gly Asn Pro Pro Thr Asp Gly Tyr Phe Ile Phe
225          755          760          765
227 tca aaa aag act gga ttt tgg aga gac tat gga tat ggc atc acc tgt      2352
228 Ser Lys Lys Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile Thr Cys
229          770          775          780
231 att tac aaa agt gat ctt cta ggt gca ggt gga ttt gat acc tca ata      2400
232 Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr Ser Ile
233 785          790          795          800
235 caa ggc tgg gga cta gaa gat gta gat ctc tac aat aaa gtc att cta      2448
236 Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val Ile Leu
237          805          810          815
239 tct ggc tta agg cca ttc aga agc caa gaa gta gga gtg gtg cat att      2496
240 Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val His Ile
241          820          825          830
243 ttc cat cca gtt cat tgt gat cct aac ttg gac cct aag cag tat aag      2544
244 Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln Tyr Lys
245          835          840          845
247 atg tgc tta gga tcc aag gca agt act ttc gcc tca acc atg caa ctg      2592
248 Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met Gln Leu
249          850          855          860
251 gct gaa ctc tgg ctt gaa aaa cat tta ggt gtc agg tac aat cga act      2640
252 Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Tyr Asn Arg Thr
253 865          870          875          880
255 ctc tcc tga      2649
256 Leu Ser
259 <210> SEQ ID NO: 2
260 <211> LENGTH: 882

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261 <212> TYPE: PRT
262 <213> ORGANISM: Homo sapiens
264 <400> SEQUENCE: 2
265 Met Ala Val Arg Ser Arg Arg Pro Trp Met Ser Val Ala Leu Gly Leu
266 1 5 10 15
268 Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala
269 20 25 30
271 Glu Leu Ser Glu Arg Lys Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr
272 35 40 45
274 Gly Arg Ser Ala Ala Gly Pro Arg Ala Gly Ala Gln Gln Pro Leu Pro
275 50 55 60
277 Gln Pro Gln Ser Arg Pro Arg Gln Glu Gln Ser Pro Pro Ala Arg
278 65 70 75 80
280 Gln Asp Leu Gln Gly Pro Pro Leu Pro Glu Ala Ala Pro Gly Ile Thr
281 85 90 95
283 Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Pro Pro Leu Gln Arg
284 100 105 110
286 Arg Arg Gly Arg Glu Pro Glu Gly Ala Thr Gly Leu Pro Gly Ala Pro
287 115 120 125
289 Ala Ala Glu Gly Glu Pro Glu Glu Glu Asp Gly Gly Ala Ala Gly Gln
290 130 135 140
292 Arg Arg Asp Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly
293 145 150 155 160
295 Gly Ala Ala Ala Pro Ser Ala Arg Pro Arg Asp Phe Leu Tyr Val Gly
296 165 170 175
298 Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln
299 180 185 190
301 Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser
302 195 200 205
304 Gln Gln Pro Pro Asn Ala Gly Gln Pro Pro Pro Pro Leu Pro Val Ile
305 210 215 220
307 Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe
308 225 230 235 240
310 Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu Trp
311 245 250 255
313 Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Lys Leu Glu
314 260 265 270
316 Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu Gly Gln
317 275 280 285
319 Thr Gly Leu Gly Asn Ile Glu Glu Leu Gly Lys Leu Gly Leu Glu Pro
320 290 295 300
322 Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser Arg Glu
323 305 310 315 320
325 Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg Glu Met
326 325 330 335
328 Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg Arg Phe
329 340 345 350
331 Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu Phe His
332 355 360 365

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Wrong Format